



Rec'd PCT/PTO 22 MAR 2002 #6

SEQUENCE LISTING

<110> Cahoon, Rebecca E.
Lee, Jian-Ming
Tao, Youn

<120> PLANT 1-DEOXY-D-XYLULOSE 5-PHOSPHATE REDUCTOISOMERASE

<130> BB-1297

<140> US/09/857,557
<141> 2001-09-22

<150> 60/110,865
<151> 1998-12-04

<160> 22

<170> Microsoft Office 97

<210> 1
<211> 565
<212> DNA
<213> Zea mays

<220>
<221> unsure
<222> (5)..(9)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (450)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (549)
<223> n = A, C, G, or T

<400> 1
aatgnnnnna tcaggctgtt acataggggg gttgcattg tacacaccca acctggccta 60
gcctacccta ctacactcggtccgg caccggcggc gacggtcgcc accaccgctc 120
ccctccctct ccccttcctc gcccagcggc aattaccaca gcctccccag caagccggga 180
tggctgcact caaggcatcg ttccgggggtg agctcagcgc cgcttccttc ctcgactcca 240
gcaggggacc tctcgccag cacaaggatgg attttacgtt tcaaaggaag ggcaaacgag 300
ctatttcaact gagaaggaca tgctgttcta tgcaacagac tccaccacca gcatggcctg 360
ggcgagctgt tgctgagcct ggccggagtc atgggatgac ccaaagccta tctcgattgt 420
tggttcaact ggtccatag gaacacagan attggacatt gttgcggaga atcctgataa 480
gttcagagtt gttgcttgc ctgctggatc caatgtcacg cttcttagctg atcaggtcaa 540
aacattcana ccttaagtgg ttcgg 565

<210> 2
<211> 63
<212> PRT
<213> Zea mays

<220>
<221> UNSURE
<222> (25)

<223> Xaa = ANY AMINO ACID

<220>

<221> UNSURE

<222> (58)

<223> Xaa = ANY AMINO ACID

<400> 2

Ala Trp Pro Glu Ser Trp Asp Gly Pro Lys Pro Ile Ser Ile Val Gly
1 5 10 15

Ser Thr Gly Ser Ile Gly Thr Gln Xaa Leu Asp Ile Val Ala Glu Asn
20 25 30

Pro Asp Lys Phe Arg Val Val Ala Leu Ala Ala Gly Ser Asn Val Thr
35 40 45

Leu Leu Ala Asp Gln Val Lys Thr Phe Xaa Pro Lys Leu Val Arg
50 55 60

<210> 3

<211> 868

<212> DNA

<213> Zea mays

<220>

<221> unsure

<222> (343)

<223> n = A, C, G, or T

<220>

<221> unsure

<222> (356)

<223> n = A, C, G, or T

<220>

<221> unsure

<222> (367)

<223> n = A, C, G, or T

<220>

<221> unsure

<222> (789)

<223> n = A, C, G, or T

<220>

<221> unsure

<222> (862)

<223> n = A, C, G, or T

<400> 3

gatgaatga aagaaggcattt ggctgattgc gaagagaagc cagaaattat tcctggggag 60
caaggtgtca tagaagttgc tcgccatcca gatcagttta cagttgtcac agggatagta 120
ggtttgtcag ggctgaagcc tacagttgct gcaattgaag ctggtaaaga catagcattt 180
gcaaacaacaaag agacacttat tgcagggtgtt ctttttgtc ttcccccttgc acacaaaacac 240
aaagtaaaaa ttcttccagc tgattctgag cactctgcaa tatttcagtg tataacaaggc 300
ttgtccgaag gtgcacttcg tcgcattatt ctaactgcat cangtggtgc tttcanggac 360
tggccanttg acaggctgaa agatgtaaaa gttgctgacg cttaaaagca tccaaactgg 420
aatatgggaa ggaagatcac agtagattct gctactttat tcaacaaggg tttagaagtt 480
attgaagcac attatttattt tggtgctgaa tatgatgaca ttgagattgt gattcaccca 540

cagtctatca tacactctat ggttggaaacc caggattcat ctgtccttagc tcagttggga 600
tggccagata tgccggttacc aatcttatac accttatcat gccagatag gagtcctgag 660
cgctgctaat gagaaggccg tggagttgtt cattgacgag aagattagct acctggacat 720
attcaagggtg gtggagctta catgtaacgc gcacggaaac agctggtaac aaccgtcact 780
ggaggaatng tcattacatc gtggcaagaa tatgcagcat cacaacatct ctggctgagc 840
tgtcctgcat atagtctcac anacttgt 868

<210> 4
<211> 217
<212> PRT
<213> Zea mays

<220>
<221> UNSURE
<222> (115)
<223> Xaa = ANY AMINO ACID

<220>
<221> UNSURE
<222> (119)
<223> Xaa = ANY AMINO ACID

<220>
<221> UNSURE
<222> (123)
<223> Xaa = ANY AMINO ACID

<400> 4
Asp Glu Leu Lys Glu Ala Leu Ala Asp Cys Glu Glu Lys Pro Glu Ile
1 5 10 15

Ile Pro Gly Glu Gln Gly Val Ile Glu Val Ala Arg His Pro Asp Ala
20 25 30

Val Thr Val Val Thr Gly Ile Val Gly Cys Ala Gly Leu Lys Pro Thr
35 40 45

Val Ala Ala Ile Glu Ala Gly Lys Asp Ile Ala Leu Ala Asn Lys Glu
50 55 60

Thr Leu Ile Ala Gly Gly Pro Phe Val Leu Pro Leu Ala His Lys His
65 70 75 80

Lys Val Lys Ile Leu Pro Ala Asp Ser Glu His Ser Ala Ile Phe Gln
85 90 95

Cys Ile Gln Gly Leu Ser Glu Gly Ala Leu Arg Arg Ile Ile Leu Thr
100 105 110

Ala Ser Xaa Gly Ala Phe Xaa Asp Trp Pro Xaa Asp Arg Leu Lys Asp
115 120 125

Val Lys Val Ala Asp Ala Leu Lys His Pro Asn Trp Asn Met Gly Arg
130 135 140

Lys Ile Thr Val Asp Ser Ala Thr Leu Phe Asn Lys Gly Leu Glu Val
145 150 155 160

Ile Glu Ala His Tyr Leu Phe Gly Ala Glu Tyr Asp Asp Ile Glu Ile
165 170 175

Val Ile His Pro Gln Ser Ile Ile His Ser Met Val Glu Thr Gln Asp
180 185 190

Ser Ser Val Leu Ala Gln Leu Gly Trp Pro Asp Met Arg Leu Pro Ile
195 200 205

Leu Tyr Thr Leu Ser Trp Pro Asp Arg
210 215

<210> 5
<211> 1901
<212> DNA
<213> Oryza sativa

<400>	5					
acactatgac	catgattacg	ccaagcgcgc	aattaaccct	cactaaaggg	aacaaaagct	60
ggagctccac	cgccgtggcg	gccgcctctag	aactagtgg	tcccccgggc	tgcagaatt	120
cgccacgagg	tttaaaccag	acgtcgagtc	gagcattaac	tcagtcaggg	tggccatggc	180
gctcaaggc	gtctcttcc	ccggggactt	ggccgcgtc	tcattcctcg	actccaaacag	240
aggaggagct	ttaaaccagc	tcaaagtgg	cctcccgtt	caaacgaggg	acagaagagc	300
agtttccctg	agaaggactt	gctgttcaat	gcaaacaggt	ccaccaccag	catggcctgg	360
tcgagccgtt	gtgaacctg	ggaggaggtc	atgggatggc	cccaaggccta	tctcaattgt	420
tggctcaacc	ggttctattt	gcacacagac	attggacata	gttgccgaga	atccagataa	480
attccgggtt	gttgctctt	ctgctggctc	caatgtgact	cttcttagctg	atcagtgaa	540
aacattcaaa	ccaaagctt	ttgctgttaag	aatatgagtc	ttagttgtat	agctaaagga	600
agccttagct	gattgtgatt	ggaagccaga	aattatttct	ggtgagcaag	gtgtcataga	660
ggttgcgc	cacccagatg	cagttacagt	tgttacttgg	atagtaggg	gtgcaggact	720
gaaggctaca	gttgctgcaa	ttgaagctgg	gaaagatata	gcattggcga	acaaagagac	780
acttatttgc	ggggctt	ttgtgcttcc	ccttgcacaa	aagcacaaaag	tgaaaataact	840
tcctgtgtat	tctgagca	ctgcttatatt	tcagtgtata	caaggcttgc	ccgaaggagc	900
acttcgcgc	attattttga	ctgcatcagg	tggtgctt	aggactggc	cagttgacaa	960
gttgaagaa	gtaaaagtt	ctgatgttt	aaagcaccc	aacttggata	tggggaaagaa	1020
gattactgt	gattctgtca	cattattcaa	caagggttta	gaagttattt	aagcacattt	1080
tttatttgtt	gttgaatacg	atgacattga	aatttgtatc	cacccacaaat	ctatcataca	1140
ctctatgatt	gaaacccagg	attcatctgt	gttggctcaa	ctgggatggc	cagatatgcg	1200
gataccaaacc	ttatacacca	tgtcttggcc	agacagaatc	tattgctcag	aggtcacctg	1260
gccccgacta	gatctttca	agctgggttc	actgacattc	aaagctcctg	acaatgtgaa	1320
atacccgtcg	atggatctcg	cctatgcagc	tggaagagct	gggggcacca	tgacaggagt	1380
tctgagtgt	gtctaatgaga	aggctgtgg	gttgttcatc	gatggaaaaga	tcgggtacct	1440
ggacatcttc	aagggtgtgg	agctgacatg	cgacgctcat	cggaatgagc	tagtaacaag	1500
gccatcaactg	gaggagatca	tacattatga	tctgtggcgc	agggagtatg	ctgcccgcct	1560
acagccatcc	actggcctca	gccctgtacc	tgtctagatc	ttttagcaat	acaaaattac	1620
agtagcattg	tacactactg	ccgtgccagc	tccatgcata	gtcagcagct	ggccactctc	1680
tagctatatc	tagatgcgag	agaattttaa	ggatgttaat	catgcctca	catgaataaa	1740
tcgttgcgtcc	gtgcgttgt	tattcatgt	aattttgacg	gatggtcaag	aaaaaataac	1800
aatggcaaat	taattttaggg	aaaaaaaaaa	aaaaaaaaact	cgaggggggg	cccggtaccc	1860
aattcgcct	atagtgagtc	gtattacgcg	cgctcactgg	c		1901

<210> 6
<211> 473
<212> PRT
<213> Oryza sativa

<400> 6
Met Ala Leu Lys Val Val Ser Phe Pro Gly Asp Leu Ala Ala Val Ser
1 5 10 15

Phe Leu Asp Ser Asn Arg Gly Gly Ala Phe Asn Gln Leu Lys Val Asp
20 25 30

Leu Pro Phe Gln Thr Arg Asp Arg Arg Ala Val Ser Leu Arg Arg Thr
 35 40 45

 Cys Cys Ser Met Gln Gln Ala Pro Pro Pro Ala Trp Pro Gly Arg Ala
 50 55 60

 Val Val Glu Pro Gly Arg Arg Ser Trp Asp Gly Pro Lys Pro Ile Ser
 65 70 75 80

 Ile Val Gly Ser Thr Gly Ser Ile Gly Thr Gln Thr Leu Asp Ile Val
 85 90 95

 Ala Glu Asn Pro Asp Lys Phe Arg Val Val Ala Leu Ala Ala Gly Ser
 100 105 110

 Asn Val Thr Leu Leu Ala Asp Gln Val Lys Thr Phe Lys Pro Lys Leu
 115 120 125

 Val Ala Val Arg Asn Glu Ser Leu Val Asp Glu Leu Lys Glu Ala Leu
 130 135 140

 Ala Asp Cys Asp Trp Lys Pro Glu Ile Ile Pro Gly Glu Gln Gly Val
 145 150 155 160

 Ile Glu Val Ala Arg His Pro Asp Ala Val Thr Val Val Thr Gly Ile
 165 170 175

 Val Gly Cys Ala Gly Leu Lys Pro Thr Val Ala Ala Ile Glu Ala Gly
 180 185 190

 Lys Asp Ile Ala Leu Ala Asn Lys Glu Thr Leu Ile Ala Gly Gly Pro
 195 200 205

 Phe Val Leu Pro Leu Ala Gln Lys His Lys Val Lys Ile Leu Pro Ala
 210 215 220

 Asp Ser Glu His Ser Ala Ile Phe Gln Cys Ile Gln Gly Leu Pro Glu
 225 230 235 240

 Gly Ala Leu Arg Arg Ile Ile Leu Thr Ala Ser Gly Gly Ala Phe Arg
 245 250 255

 Asp Trp Pro Val Asp Lys Leu Lys Glu Val Lys Val Ala Asp Ala Leu
 260 265 270

 Lys His Pro Asn Trp Asn Met Gly Lys Lys Ile Thr Val Asp Ser Ala
 275 280 285

 Thr Leu Phe Asn Lys Gly Leu Glu Val Ile Glu Ala His Tyr Leu Phe
 290 295 300

 Gly Ala Glu Tyr Asp Asp Ile Glu Ile Val Ile His Pro Gln Ser Ile
 305 310 315 320

 Ile His Ser Met Ile Glu Thr Gln Asp Ser Ser Val Leu Ala Gln Leu
 325 330 335

 Gly Trp Pro Asp Met Arg Ile Pro Thr Leu Tyr Thr Met Ser Trp Pro
 340 345 350

Asp Arg Ile Tyr Cys Ser Glu Val Thr Trp Pro Arg Leu Asp Leu Cys
 355 360 365
 Lys Leu Gly Ser Leu Thr Phe Lys Ala Pro Asp Asn Val Lys Tyr Pro
 370 375 380
 Ser Met Asp Leu Ala Tyr Ala Ala Gly Arg Ala Gly Gly Thr Met Thr
 385 390 395 400
 Gly Val Leu Ser Ala Ala Asn Glu Lys Ala Val Glu Leu Phe Ile Asp
 405 410 415
 Glu Lys Ile Gly Tyr Leu Asp Ile Phe Lys Val Val Glu Leu Thr Cys
 420 425 430
 Asp Ala His Arg Asn Glu Leu Val Thr Arg Pro Ser Leu Glu Glu Ile
 435 440 445
 Ile His Tyr Asp Leu Trp Ala Arg Glu Tyr Ala Ala Ser Leu Gln Pro
 450 455 460
 Ser Thr Gly Leu Ser Pro Val Pro Val
 465 470
 <210> 7
 <211> 1592
 <212> DNA
 <213> Glycine max
 <220>
 <221> unsure
 <222> (993)
 <223> n = A, C, G, or T
 <220>
 <221> unsure
 <222> (1402)
 <223> n = A, C, G, or T
 <400> 7
 gctggttcaa ctgaggtgat ggcttgaat ttgccttc cgcggcaagt gaagccctta 60
 tttttctttt caaataactc cacaaaaactt ccaggtagt tttctttgaa gagaaaaagat 120
 agtgacacaa cagtagagag acgagtttat tgctctgcg ctgctcaatc accaccacca 180
 gcatggccag gaacagctat tccccggcct tctgatttca agacatggga tgggcaaaaa 240
 cctatttctg tcttaggatc tacgggttca atttggaaactc agacactgag tatagtggct 300
 gagttcccaag aaagatttaa agttgtgagc ctttgtctg gctctaataat tactcttctt 360
 gctgaccaga ttaaaaacatt taagcctgaa gtttgtggc tttagaaatga gtctttaatt 420
 gatgaactca aagaggctt ggctgatgtg gatcacaaac ccgaaatcat ccctggagag 480
 caaggagtc ttgaggccgc tcgtcacccct gatgccacca ctgttagttac aggcatagtt 540
 ggttgtgcag gattaaagcc aacagttgca gcaattgaag caggaaaga catagcattg 600
 gccaacaaag agacaatgat tgccggagcc cttttgttc ttcccttgc tcacaaacat 660
 aacataaaaa ttcttcccgc tgattcgaa cattctgcaa ttttcagtc tatccagggg 720
 ttgccaaagg gtgcacttag gaaaatcctt ttaactggat caggaggtgc tttcagagaa 780
 tggcctgctg aaaagatgaa agatattaag ctttgtatg cattaaagca tcccatatgg 840
 agtttgggaa gaaaaataac tattgactct gtcaccctt tcaataaggg tctagaagta 900
 attgaagcac attactgtt tggagcaagc tatgacgata ttgagattgt tattcatcct 960
 caatccatca tacattccctt ggttggaaacg cangattcat ctgttaatgc acagttgggg 1020
 atacctgaca tgcgcttacc gtcctttat acattatctt ggccagaaag aatcttatgc 1080
 tctgaagtaa cttggcctcg tcttgatctt agcaagttatg gttctctaac attttatgca 1140

ccggatgaca agaagttcc atcggtgaat ctttgctatg ctgcgggacg tgctggaggc 1200
accatgacag gagttcttag tgcagcaaat gagaaagctg tagaaatgtt tgttgaagaa 1260
aagatttagtt atctggatat attcaagggtt gtggaactaa cttgtcagga acatcaaaag 1320
gaatttagtag catctccgtc actcgaagaa attattcact atgaccaatg ggctcgacaa 1380
tatgctgcta gtctgcaaaa angcttcaag tgtttgaatc ccataatttct gacatatttt 1440
agaagttggg gctgtgggtt attgttggca actgcttagca tattttgtaa atgtattgtt 1500
ggttcatcaa tcttgtaaaa tgtaaagggg taagctatat aaagtatatg tactcctaaa 1560
agggttcaa taaaagttct agttcaaga aa 1592

<210> 8
<211> 499
<212> PRT
<213> Glycine max

<220>
<221> UNSURE
<222> (325)
<223> Xaa = ANY AMINO ACID

<220>
<221> UNSURE
<222> (462)
<223> Xaa = ANY AMINO ACID

<400> 8
Met Ala Leu Asn Leu Pro Ser Pro Ala Gln Val Lys Pro Leu Phe Phe
1 5 10 15

Ser Ser Asn Asn Ser Thr Lys Leu Pro Gly Ser Phe Ser Leu Lys Arg
20 25 30

Lys Asp Ser Asp Thr Thr Val Glu Arg Arg Val Tyr Cys Ser Ala Ala
35 40 45

Ala Gln Ser Pro Pro Pro Ala Trp Pro Gly Thr Ala Ile Pro Glu Pro
50 55 60

Ser Asp Phe Lys Thr Trp Asp Gly Gln Lys Pro Ile Ser Val Leu Gly
65 70 75 80

Ser Thr Gly Ser Ile Gly Thr Gln Thr Leu Ser Ile Val Ala Glu Phe
85 90 95

Pro Glu Arg Phe Lys Val Val Ser Leu Ala Ala Gly Ser Asn Ile Thr
100 105 110

Leu Leu Ala Asp Gln Ile Lys Thr Phe Lys Pro Glu Val Val Gly Leu
115 120 125

Arg Asn Glu Ser Leu Ile Asp Glu Leu Lys Glu Ala Leu Ala Asp Val
130 135 140

Asp His Lys Pro Glu Ile Ile Pro Gly Glu Gln Gly Val Ile Glu Ala
145 150 155 160

Ala Arg His Pro Asp Ala Thr Thr Val Val Thr Gly Ile Val Gly Cys
165 170 175

Ala Gly Leu Lys Pro Thr Val Ala Ala Ile Glu Ala Gly Lys Asp Ile
180 185 190

Ala Leu Ala Asn Lys Glu Thr Met Ile Ala Gly Ala Pro Phe Val Leu
 195 200 205
 Pro Leu Ala His Lys His Asn Ile Lys Ile Leu Pro Ala Asp Ser Glu
 210 215 220
 His Ser Ala Ile Phe Gln Ser Ile Gln Gly Leu Pro Lys Gly Ala Leu
 225 230 235 240
 Arg Lys Ile Leu Leu Thr Gly Ser Gly Gly Ala Phe Arg Glu Trp Pro
 245 250 255
 Ala Glu Lys Met Lys Asp Ile Lys Leu Ala Asp Ala Leu Lys His Pro
 260 265 270
 Ile Trp Ser Leu Gly Arg Lys Ile Thr Ile Asp Ser Ala Thr Leu Phe
 275 280 285
 Asn Lys Gly Leu Glu Val Ile Glu Ala His Tyr Leu Phe Gly Ala Ser
 290 295 300
 Tyr Asp Asp Ile Glu Ile Val Ile His Pro Gln Ser Ile Ile His Ser
 305 310 315 320
 Leu Val Glu Thr Xaa Asp Ser Ser Val Asn Ala Gln Leu Gly Ile Pro
 325 330 335
 Asp Met Arg Leu Pro Leu Leu Tyr Thr Leu Ser Trp Pro Glu Arg Ile
 340 345 350
 Tyr Cys Ser Glu Val Thr Trp Pro Arg Leu Asp Leu Ser Lys Tyr Gly
 355 360 365
 Ser Leu Thr Phe Tyr Ala Pro Asp Asp Lys Lys Phe Pro Ser Val Asn
 370 375 380
 Leu Cys Tyr Ala Ala Gly Arg Ala Gly Gly Thr Met Thr Gly Val Leu
 385 390 395 400
 Ser Ala Ala Asn Glu Lys Ala Val Glu Met Phe Val Glu Glu Lys Ile
 405 410 415
 Ser Tyr Leu Asp Ile Phe Lys Val Val Glu Leu Thr Cys Gln Glu His
 420 425 430
 Gln Lys Glu Leu Val Ala Ser Pro Ser Leu Glu Glu Ile Ile His Tyr
 435 440 445
 Asp Gln Trp Ala Arg Gln Tyr Ala Ala Ser Leu Gln Lys Xaa Phe Lys
 450 455 460
 Cys Leu Asn Pro Ile Phe Leu Thr Tyr Phe Arg Ser Trp Gly Cys Gly
 465 470 475 480
 Gly Leu Leu Ala Thr Ala Ser Ile Phe Cys Lys Cys Ile Val Gly Ser
 485 490 495
 Ser Ile Leu

<210> 9
<211> 784
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (55)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (100)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (109)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (120)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (659)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (675)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (721)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (735)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (740)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (743)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (756)
<223> n = A, C, G, or T

```

<220>
<221> unsure
<222> (772)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (779)..(780)
<223> n = A, C, G, or T

<400> 9
gcacgggtt attgctcagt gcaggcaaca ccaccaccac cagcctggcc gggangagcg 60
gttccggAAC aaggTCGCAA gacttggat ggaccaaaan ccatttcant tttggggagn 120
actggttcaa ttggaactca gacactagat attgtggcag agaatccaga taagttaaa 180
gttggcAC ttgcagCTGG ttcaaATGTT actcttctt cagaccaggt aaaaagattt 240
aaggCCTCAAC ttgttgCTGT tagaaatgag tccctaattt ctgaacttga agaggccttG 300
catgatgttG aagaaaaacc tgagatcatc cctggagAGC agggaatcat tgaggTTGCT 360
cgTCACCCAG atgcAGTtag ttttagtca GGAATAGTAG GCTGTGcAGG ACTGAAGCCA 420
acAGTTGcAG CGATAGAAGC AGGGAAAGAC ATAGCTTGG CCAACAAAGA GACATTGATT 480
gCTGGAGGTC CTTGTTCTC CTCTTGCTCA GAAGCATAAT GTAAAAATAC TTCCAGCTGA 540
ttcagaacat ctgccatctt tcagtgtatc caggggttgc cagagggtgc acttaggaga 600
gttattttaa ctgcatctgg aggtgcttC AGGGGATGc CAGTGGATA ACTGAAGANG 660
ttaaagtgc tgatncatta aaacatccta ctggaatatg gggaaaagaa ctgtggactc 720
ngcaacctt taaanaaggn canaagtaaa tgagcncata ctgtttggg cngctaagnn 780
catt 784

<210> 10
<211> 215
<212> PRT
<213> Glycine max

<220>
<221> UNSURE
<222> (19)
<223> Xaa = ANY AMINO ACID

<220>
<221> UNSURE
<222> (183)
<223> Xaa = ANY AMINO ACID

<400> 10
Ala Arg Val Tyr Cys Ser Val Gln Ala Thr Pro Pro Pro Pro Ala Trp
 1           5           10          15

Pro Gly Xaa Ala Val Pro Glu Gln Gly Arg Lys Thr Trp Asp Gly Pro
 20          25          30

Lys Pro Ile Ser Ile Val Gly Ser Thr Gly Ser Ile Gly Thr Gln Thr
 35          40          45

Leu Asp Ile Val Ala Glu Asn Pro Asp Lys Phe Lys Val Val Ala Leu
 50          55          60

Ala Ala Gly Ser Asn Val Thr Leu Leu Ala Asp Gln Val Lys Arg Phe
 65          70          75          80

Lys Pro Gln Leu Val Ala Val Arg Asn Glu Ser Leu Ile Ala Glu Leu
 85          90          95

```

Glu Glu Ala Leu His Asp Val Glu Glu Lys Pro Glu Ile Ile Pro Gly
 100 105 110

Glu Gln Gly Ile Ile Glu Val Ala Arg His Pro Asp Ala Val Ser Val
 115 120 125

Val Thr Gly Ile Val Gly Cys Ala Gly Leu Lys Pro Thr Val Ala Ala
 130 135 140

Ile Glu Ala Gly Lys Asp Ile Ala Leu Ala Asn Lys Glu Thr Leu Ile
 145 150 155 160

Ala Gly Gly Pro Leu Ser Pro Leu Ala Gln Lys His Asn Val Lys Ile
 165 170 175

Leu Pro Ala Asp Ser Asp Xaa Ser Ala Ile Phe Gln Cys Ile Gln Gly
 180 185 190

Leu Pro Glu Gly Ala Leu Arg Arg Val Ile Leu Thr Ala Ser Gly Gly
 195 200 205

Ala Phe Arg Gly Trp Pro Val
 210 215

<210> 11
 <211> 642
 <212> DNA
 <213> Triticum aestivum

<220>
 <221> unsure
 <222> (506)
 <223> n = A, C, G, or T

<220>
 <221> unsure
 <222> (516)
 <223> n = A, C, G, or T

<220>
 <221> unsure
 <222> (534)
 <223> n = A, C, G, or T

<220>
 <221> unsure
 <222> (554)
 <223> n = A, C, G, or T

<220>
 <221> unsure
 <222> (576)
 <223> n = A, C, G, or T

<220>
 <221> unsure
 <222> (584)
 <223> n = A, C, G, or T

```

<220>
<221> unsure
<222> (597)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (601)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (606)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (625)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (628)
<223> n = A, C, G, or T

<400> 11
ctccttcctcc ctcctcgagc ttcctccgg caccaccagg agcaggaggg gagccgcctt 60
ccgccccccgc cagcaccaggc gcaaagtgcga cttcacatat caaaggaggg acaaaaagagc 120
tgcctacctg aggacatgct gctccatgca gcagggccca ccgcccgcct ggccaggccg 180
agccgtcggt gaaacctgaga ggaggtcggt ggagggccca aagcccatct ccatcgtcgg 240
ctcaaccggc tccatagggaa cacagacatt ggacatcggt gcggagaacc tgacaagttc 300
ccgggttgtc gcccttgctg ctgggtccaa cgtcactcct ctagctgata aggtgaaaac 360
gttcaaacca aactgggtgg tgttaagaaa cgatccatia cttaacgagc taaaggaagc 420
attaactggt tggaaagag atccggatta tccctgggaa caagtgcata gaggcgcacc 480
caccggacc attacatcct tacggnatat aggttncaag atcaacctac attncaacat 540
ttaactggaa aatntgctt gggaaacaaaa accttnccag gtgnccctct ctcctncca 600
naacanattt aaatactctg cgatnaanat ctgatatatcat ga 642

<210> 12
<211> 94
<212> PRT
<213> Triticum aestivum

<400> 12
Met Gln Gln Gly Pro Pro Pro Ala Trp Pro Gly Arg Ala Val Val Glu
1 5 10 15

Pro Glu Arg Arg Ser Trp Glu Gly Pro Lys Pro Ile Ser Ile Val Gly
20 25 30

Ser Thr Gly Ser Ile Gly Thr Gln Thr Leu Asp Ile Val Ala Glu Asn
35 40 45

Leu Thr Ser Ser Arg Val Val Ala Leu Ala Ala Gly Ser Asn Val Thr
50 55 60

Pro Leu Ala Asp Lys Val Lys Thr Phe Lys Pro Asn Trp Val Val Leu
65 70 75 80

Arg Asn Asp Pro Leu Leu Asn Glu Leu Lys Glu Ala Leu Thr

```

85

90

<210> 13
<211> 360
<212> DNA
<213> Triticum aestivum

<220>
<221> unsure
<222> (295)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (299)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (313)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (338)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (352)
<223> n = A, C, G, or T

<400> 13
catctgtcct ggctcagctg gnatggcctg acatgcggct accaatcccta tacaccctgt 60
cttggccaga tagagtctac tgctccgagg tcacctggcc tcggcttagat ctttgcaagc 120
tgggctcgct gacattcaaa gctcccgaca acgtgaaata cccatcggtta gatctccgccc 180
gtacgcggca gggcgagccg ggggcaccat gacgggattt ttgagtgctg ctaatgagaa 240
ggcgtggagc ttgttcatcg acgaaaagat taactacctt ggacatcttc aaggngggng 300
agaataccctt ttnacgccaa ccgcaacaac tgggtganag ctcctccccca angggggggg 360

<210> 14
<211> 93
<212> PRT
<213> Triticum aestivum

<220>
<221> UNSURE
<222> (59)
<223> Xaa = ANY AMINO ACID

<400> 14
Ser Val Leu Ala Gln Leu Gly Trp Pro Asp Met Arg Leu Pro Ile Leu
1 5 10 15

Tyr Thr Leu Ser Trp Pro Asp Arg Val Tyr Cys Ser Glu Val Thr Trp
20 25 30

Pro Arg Leu Asp Leu Cys Lys Leu Gly Ser Leu Thr Phe Lys Ala Pro
35 40 45

Asp Asn Val Lys Tyr Pro Ser Val Asp Leu Xaa Xaa Tyr Ala Ala Gly
50 55 60

Arg Ala Gly Gly Thr Met Thr Gly Phe Leu Ser Ala Ala Asn Glu Lys
65 70 75 80

Ala Trp Ser Leu Phe Ile Asp Glu Lys Ile Asn Tyr Leu
85 90

<210> 15
<211> 1847
<212> DNA
<213> Zea mays

<220>
<221> unsure
<222> (5)..(9)
<223> n = A, C, G, or T

<400> 15
aatgnnnnna tcaggctgtt acataggggg gcttgcatgg tacacaccca acctggccta 60
gcctacccta ctacactcggtt gcccattcggtt caccggcaccg gacggtcggcc accaccgctc 120
ccctccctctt cccctccctt gcccagcggtt aattaccaca gcctcccttca agggccggga 180
tggctgcactt caaggcatcg ttccgggggtt agctcagcgcc cgcttccttc ctcgactcc 240
gcaggggacc tctcgtccatgg cacaaggatgg attttacgtt tcaaaggaaag ggccaaacgag 300
ctatttcaactt gagaaggaca tgctgttctt tgcaacacaggc tccaccacca gcatggcctt 360
ggcgagctgt tgctgagcctt ggcggaggtt catggatgg cccaaagcctt atctcgattt 420
ttgggttcaac ttgggtccata ggaacacaga cattggacat ttggcgaggaaatccctgata 480
agttcagagt ttggctgttctt gctgctggat ccaatgtcac gcttcttagt gatcaggatca 540
aaacattcaa acctaaggatgg gttgctgttaa gaaacgaatc attagtttatg gaattgaaaag 600
aaggccttggc tgatttgcgaa gagaagccatgg aaattattcc tggggagca ggtgtcatag 660
aagttgcgtcg ccattccatgg gcatgttacatg ttgtcacagg gatagtaggt ttggcgaggc 720
tgaaggcttac agttgcgtca attgaagctt gtaaaggacat agcattggca aacaaagaga 780
cacttatttgc aggtggcttcc ttgtgttcc cccttgcaca caaacacaaa gtggaaattt 840
ttccagctgtt ttctgagcactt tctgcaatatttcc ttcagtgtat acaaggctt gtcggaaatgtt 900
cacttcgtcg cattatttca actgcacatgg gtgggtctt cagggactgg ccagttgaca 960
ggctgaaaga tgtaaaaggatgg gctgacgtttaaaggatcc aaactggat atgggaagga 1020
agatcacatggt agattctgttctt acaagggtt agaagtttatttgaagcattt 1080
atttatttgg tgctgaatatttgcatggatggt gatggatggt tcaccacatgg tctatcata 1140
actctatggt tgaaaccatgg gattcatctt tccttagctca gttggatgg ccagatatgc 1200
ggttaccaat ttatcatggc cagatagaat ctattgtctt gaggtcacctt 1260
ggccccgtctt ggatcttgc aagttgggtt cactgacattt cagagcttca gacaacgtt 1320
aataaccatc aatggaccta gcctatgcgtt ctggccgcgc tggggcacc atgacaggag 1380
tcctgagcgc tgctaatgg aaggccgtgg agttgttcat ttggcgaggatgg attagctacc 1440
tggacatattt caagggtggg gatgttacat gtaacgcgc tggaaacggatgg ctggtaacaa 1500
gcccgttactt ggaggagatc gtccattacat atctgtggc gaggagatgg gcagccatgc 1560
tacaaccatc ttctggcctt agccctgttcc ctgcataata ggtcgatccac gacaacgttgt 1620
acagcaggag ttctaaatggat ttatgtgtttt gttggcttcc tttccatgtt caatttcag 1680
gcctccacat gaataaaaatgg catctatttcc atgtgattttt ttttatggat gaagtgtgcg 1740
aagtgggttgg gaaatcagat gcatccctt cgggtggatgg cttacgttgg gttgagcagc 1800
attttttaaa aaggtttttt tacctctgca aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa 1847

<210> 16
<211> 472
<212> PRT
<213> Zea mays

<400> 16
Met Ala Ala Leu Lys Ala Ser Phe Arg Gly Glu Leu Ser Ala Ala Ser
1 5 10 15

Phe Leu Asp Ser Ser Arg Gly Pro Leu Val Gln His Lys Val Asp Phe
 20 25 30

 Thr Phe Gln Arg Lys Gly Lys Arg Ala Ile Ser Leu Arg Arg Thr Cys
 35 40 45

 Cys Ser Met Gln Gln Ala Pro Pro Pro Ala Trp Pro Gly Arg Ala Val
 50 55 60

 Ala Glu Pro Gly Arg Arg Ser Trp Asp Gly Pro Lys Pro Ile Ser Ile
 65 70 75 80

 Val Gly Ser Thr Gly Ser Ile Gly Thr Gln Thr Leu Asp Ile Val Ala
 85 90 95

 Glu Asn Pro Asp Lys Phe Arg Val Val Ala Leu Ala Ala Gly Ser Asn
 100 105 110

 Val Thr Leu Leu Ala Asp Gln Val Lys Thr Phe Lys Pro Lys Leu Val
 115 120 125

 Ala Val Arg Asn Glu Ser Leu Val Asp Glu Leu Lys Glu Ala Leu Ala
 130 135 140

 Asp Cys Glu Glu Lys Pro Glu Ile Ile Pro Gly Glu Gln Gly Val Ile
 145 150 155 160

 Glu Val Ala Arg His Pro Asp Ala Val Thr Val Val Thr Gly Ile Val
 165 170 175

 Gly Cys Ala Gly Leu Lys Pro Thr Val Ala Ala Ile Glu Ala Gly Lys
 180 185 190

 Asp Ile Ala Leu Ala Asn Lys Glu Thr Leu Ile Ala Gly Gly Pro Phe
 195 200 205

 Val Leu Pro Leu Ala His Lys His Lys Val Lys Ile Leu Pro Ala Asp
 210 215 220

 Ser Glu His Ser Ala Ile Phe Gln Cys Ile Gln Gly Leu Ser Glu Gly
 225 230 235 240

 Ala Leu Arg Arg Ile Ile Leu Thr Ala Ser Gly Gly Ala Phe Arg Asp
 245 250 255

 Trp Pro Val Asp Arg Leu Lys Asp Val Lys Val Ala Asp Ala Leu Lys
 260 265 270

 His Pro Asn Trp Asn Met Gly Arg Lys Ile Thr Val Asp Ser Ala Thr
 275 280 285

 Leu Phe Asn Lys Gly Leu Glu Val Ile Glu Ala His Tyr Leu Phe Gly
 290 295 300

 Ala Glu Tyr Asp Asp Ile Glu Ile Val Ile His Pro Gln Ser Ile Ile
 305 310 315 320

 His Ser Met Val Glu Thr Gln Asp Ser Ser Val Leu Ala Gln Leu Gly
 325 330 335

Trp Pro Asp Met Arg Leu Pro Ile Leu Tyr Thr Leu Ser Trp Pro Asp
 340 345 350
 Arg Ile Tyr Cys Ser Glu Val Thr Trp Pro Arg Leu Asp Leu Cys Lys
 355 360 365
 Leu Gly Ser Leu Thr Phe Arg Ala Pro Asp Asn Val Lys Tyr Pro Ser
 370 375 380
 Met Asp Leu Ala Tyr Ala Ala Gly Arg Ala Gly Gly Thr Met Thr Gly
 385 390 395 400
 Val Leu Ser Ala Ala Asn Glu Lys Ala Val Glu Leu Phe Ile Asp Glu
 405 410 415
 Lys Ile Ser Tyr Leu Asp Ile Phe Lys Val Val Glu Leu Thr Cys Asn
 420 425 430
 Ala His Arg Asn Glu Leu Val Thr Ser Pro Ser Leu Glu Glu Ile Val
 435 440 445
 His Tyr Asp Leu Trp Ala Arg Arg Tyr Ala Ala Ser Leu Gln Pro Ser
 450 455 460
 Ser Gly Leu Ser Pro Val Pro Ala
 465 470

<210> 17
 <211> 2019
 <212> DNA
 <213> Glycine max

<400> 17
 gcagccacca ttattgttgt tattggagat ttcaattctt tgtctttcaa actcctcaag 60
 ttgggtttat gtgatgatgg ctctcaacat ctcttctcca gctgaagtca agtccathtt 120
 tttcgctgat tccttcagaat ctaactgcct cacagcaaaa ttctcagggtg ggtttgcttt 180
 taagagaaaa gagcgttagag cagcatctgg aggacgggtt tattgctcag tgccaggaaac 240
 accaccacca ccagcctggc cgggacgagc gttccggaa caagtcgca agacttggga 300
 tggaccaaaa cccatattcaa ttgtggggag tactggttca attgaaactc agacactaga 360
 tattgtggca gagaatccag ataagttaa agttgtggca cttgcagctg gttcaaatgt 420
 tacttttctt gcagaccagg taaaaagatt taagcctcaa cttgttgcgtt tttagaaatga 480
 gtcctctaatt gctgaacttg aagaggcctt gcatgatgtt gaagaaaaac ctgagatcat 540
 ccctggagag caggaaatca ttgagggtgc tcgtcacccca gatgcagttt gtgtagtcac 600
 aggaataatgtt ggttgtgcag gactgaagcc aacagtttca gcgatagaag cagggaaaga 660
 catagcttttgc ccaacaaag agacattgtat tgctggaggtt cctttgttcc ttccctcttgc 720
 tcagaagcat aatgtaaaaaa tacttccagc tgattcagaa catttcgcac tctttcaatgt 780
 tatccaggggg ttgccagagg gtgcacttag gagagtattt ttaactgcac ctggaggtgc 840
 tttcagggtt tggccagttt ataaactgaa agatgttaaa gttgtgtatg cattaaaaaca 900
 tcctaacttgg aatatggggaaaagataaac tggacttgc gtcacccctt ttaataaagg 960
 tctagaagta attgaagcac attacttggt tggagctgac tacgatcata ttgagatgtt 1020
 cattcatcca caatcaatca tacattcaat gattgaaaca caggattcat ctgttcttgc 1080
 acaattgggg tggccgtata tgcgtttgcc aatccttcat acattatcat ggcctgacag 1140
 gatttatgt tctgaagtca cttggccacg cttgtatctt tgcaagcttgc gttcaacttac 1200
 atttaaaactt ccagataatgt taaagtatcc atccatgaat cttgcatttt ctgctggccg 1260
 tgctggaggc acaatgacag gagttcttag tgcagcaat gaaaaagctg tagagatgtt 1320
 tattgtatgaa aagataagctt attggaattt attcaaaatgtt gttggagctaa catgtgagaa 1380
 gcatcaaaat gaattggat cctcttc ctttgaggaa attattcaat atgacctgtg 1440
 ggcgcgaaaa tatgctgcta gtctgcaaga ctcttccacgc ttcaactccta ttcttgcatg 1500
 aggtatgatta aacttagggat gtggctgtatc cttcccaattt gcccatttgc accataattt 1560

cttcgggcat tgaacaatgt agaatggtgc attccacaga tggtaaaaat taaataggtt 1620
ttttgtttat ggaatgttgg ttttttaaca ctttcaatt gatcttatag ttttgcgtt 1680
atttcatgga aaacgatgtc ttttaatag tcaataggag cctaggaggt tggttgggt 1740
cctatgaatg tgtcaaagtc aagaagggga atggatttc tcataatcaa aatttacatg 1800
atgtggtcaa ctagaagttt tgtatttctc ttttctaata agaattaaat aggtggagtc 1860
ttacaaaaat taacagagat agacacaaaa gttgaccaat caccatcac tttcataaaaa 1920
ggattccccc tcttttccct cagcacacat tcgttggctg atattattat atgaaattgg 1980
tattatttgg atatcatagc taaaaaaaaa aaaaaaaaaa 2019

<210> 18
<211> 475
<212> PRT
<213> Glycine max

<400> 18
Met Met Ala Leu Asn Ile Ser Ser Pro Ala Glu Val Lys Ser Ile Phe
1 5 10 15

Phe Ala Asp Ser Phe Lys Ser Asn Cys Leu Thr Ala Lys Phe Ser Gly
20 25 30

Gly Phe Ala Phe Lys Arg Lys Glu Arg Arg Ala Ala Ser Gly Gly Arg
35 40 45

Val Tyr Cys Ser Val Gln Ala Thr Pro Pro Pro Ala Trp Pro Gly
50 55 60

Arg Ala Val Pro Glu Gln Gly Arg Lys Thr Trp Asp Gly Pro Lys Pro
65 70 75 80

Ile Ser Ile Val Gly Ser Thr Gly Ser Ile Gly Thr Gln Thr Leu Asp
85 90 95

Ile Val Ala Glu Asn Pro Asp Lys Phe Lys Val Val Ala Leu Ala Ala
100 105 110

Gly Ser Asn Val Thr Leu Leu Ala Asp Gln Val Lys Arg Phe Lys Pro
115 120 125

Gln Leu Val Ala Val Arg Asn Glu Ser Leu Ile Ala Glu Leu Glu Glu
130 135 140

Ala Leu His Asp Val Glu Glu Lys Pro Glu Ile Ile Pro Gly Glu Gln
145 150 155 160

Gly Ile Ile Glu Val Ala Arg His Pro Asp Ala Val Ser Val Val Thr
165 170 175

Gly Ile Val Gly Cys Ala Gly Leu Lys Pro Thr Val Ala Ala Ile Glu
180 185 190

Ala Gly Lys Asp Ile Ala Leu Ala Asn Lys Glu Thr Leu Ile Ala Gly
195 200 205

Gly Pro Phe Val Leu Pro Leu Ala Gln Lys His Asn Val Lys Ile Leu
210 215 220

Pro Ala Asp Ser Glu His Ser Ala Ile Phe Gln Cys Ile Gln Gly Leu
225 230 235 240

Pro Glu Gly Ala Leu Arg Arg Val Ile Leu Thr Ala Ser Gly Gly Ala
 245 250 255
 Phe Arg Asp Trp Pro Val Asp Lys Leu Lys Asp Val Lys Val Ala Asp
 260 265 270
 Ala Leu Lys His Pro Asn Trp Asn Met Gly Lys Lys Ile Thr Val Asp
 275 280 285
 Ser Ala Thr Leu Phe Asn Lys Gly Leu Glu Val Ile Glu Ala His Tyr
 290 295 300
 Leu Phe Gly Ala Asp Tyr Asp His Ile Glu Ile Val Ile His Pro Gln
 305 310 315 320
 Ser Ile Ile His Ser Met Ile Glu Thr Gln Asp Ser Ser Val Leu Ala
 325 330 335
 Gln Leu Gly Trp Pro Asp Met Arg Leu Pro Ile Leu Tyr Thr Leu Ser
 340 345 350
 Trp Pro Asp Arg Ile Tyr Cys Ser Glu Val Thr Trp Pro Arg Leu Asp
 355 360 365
 Leu Cys Lys Leu Gly Ser Leu Thr Phe Lys Thr Pro Asp Asn Val Lys
 370 375 380
 Tyr Pro Ser Met Asn Leu Ala Phe Ser Ala Gly Arg Ala Gly Thr
 385 390 395 400
 Met Thr Gly Val Leu Ser Ala Ala Asn Glu Lys Ala Val Glu Met Phe
 405 410 415
 Ile Asp Glu Lys Ile Ser Tyr Trp Asn Leu Phe Lys Val Val Glu Leu
 420 425 430
 Thr Cys Glu Lys His Gln Asn Glu Leu Val Ser Ser Pro Ser Leu Glu
 435 440 445
 Glu Ile Ile His Tyr Asp Leu Trp Ala Arg Lys Tyr Ala Ala Ser Leu
 450 455 460
 Gln Asp Ser Ser Ser Phe Thr Pro Ile Leu Ala
 465 470 475
 <210> 19
 <211> 1640
 <212> DNA
 <213> Triticum aestivum
 <400> 19
 gcacgagctc cttctccctc ctcgagctct cctccggcac caccaggagc aggaggggag 60
 ccgccttccg cccccgcccag caccagcgca aagtggactt gacgttcaa aggagggaca 120
 aaagagcagc ctacctgagg acatgctgct cgatgcagca gggcccacccg cccgcctggc 180
 ctggccgagc cgtcgccgaa cccgagagga ggtcgtggga gggccccaaag cccatctcga 240
 tcgtcggctc aaccggttcc ataggaacac agacattgga catcggtcg gagaatcctg 300
 acaagttccg gttgtcgct cttgctgctg gctccaatgt cactttcta gctgatcagg 360
 tgaaaacgtt caagccaaag ctggtggtcg taagaaaacga gtcattactt aacgagctaa 420
 aggaagcgtt agctgggtgt gaagaaatgc cggaaattat tcctggggag caaggtgtca 480
 tagaggtcgc tcgccacccg gatgcagttac cagtcgttac gggcatagta gggtgtcag 540

gactcaagcc tacagttgca gcaattgaag ctggaaaga tattgcgtt gcgaacaaag 600
 agacacttat cgcaggcggt ccgttcgtgc ttccccttgc gcacaagcac aatgtaaaaa 660
 tacttcctgc tgattcagag cactctgcaa tatttcagtg tatacaaggc ttgtctgaag 720
 gatcacttcg tcgcgttatt ctgactgcgt ctggcgggtc tttcagggac tggccagttg 780
 agaagctgaa agatgtaaag gttgccatg ctttgaagca cccaaactgg agcatgggaa 840
 agaaaatcac agtagattct gctactttgt tcaacaaggc gttagaagtt atcgaggcgc 900
 attatttgtt tggctgtaa tatgatgaca ttgagattgt gattcaccca cagtccatca 960
 tacactctat gattgaaacc caggattcat ctgtcctgac tcagctggaa tggccagaca 1020
 tgccgctacc gatcctatac accttgttctt ggccagaccg agtctactgc tccgaggta 1080
 cctggccccg gctagacctt tgcaagctgg gttcgctgac atttaaagct cccgacaacg 1140
 taaaaatcccc atcggtggat ctcgcgtatg cggcaggggcg ggccgggggc accatgacgg 1200
 gagttttgag tgctgtaat gagaaggcgg tggagctgtt catgcacgaa aagatcagct 1260
 acctggacat cttcaaggtg gtggagatga cgtgcacgc gcaccgcaac gagctggta 1320
 caaggccgtc gctcgaggag atcatacatt acgaccagtg ggcaaggaag tttgcccca 1380
 acctacagcc atcgctgtct ggacggagcc ctgtgctgac ctaaggccct tttcctgga 1440
 gctggccgat gaagcacaga agatgttagcc atggcctgac cttgtaaaaa ctggccatgt 1500
 gaaaaaccaaag ctttagatatt tcaacaaggc acacatagt tgccttccag aaatgttaat 1560
 catgtgttgg cacgataaa tcatgttaagt tttgatggat ggatgaaata ggcaaggaat 1620
 caaaaaaaaaaaaaaa aaaaaaaaaaaaaaa 1640

<210> 20

<211> 473

<212> PRT

<213> *Triticum aestivum*

<400> 20

Thr	Ser	Ser	Phe	Ser	Leu	Leu	Glu	Leu	Ser	Ser	Gly	Thr	Thr	Arg	Ser
1					5				10				15		

Arg	Arg	Gly	Ala	Ala	Phe	Arg	Pro	Arg	Gln	His	Gln	Arg	Lys	Val	Asp
					20				25				30		

Leu	Thr	Phe	Gln	Arg	Arg	Asp	Lys	Arg	Ala	Ala	Tyr	Leu	Arg	Thr	Cys
						35		40					45		

Cys	Ser	Met	Gln	Gln	Gly	Pro	Pro	Pro	Ala	Trp	Pro	Gly	Arg	Ala	Val
						50		55				60			

Ala	Glu	Pro	Glu	Arg	Arg	Ser	Trp	Glu	Gly	Pro	Lys	Pro	Ile	Ser	Ile
						65		70			75				80

Val	Gly	Ser	Thr	Gly	Ser	Ile	Gly	Thr	Gln	Thr	Leu	Asp	Ile	Val	Ala
						85			90				95		

Glu	Asn	Pro	Asp	Lys	Phe	Arg	Val	Val	Ala	Leu	Ala	Gly	Ser	Asn
						100		105				110		

Val	Thr	Leu	Leu	Ala	Asp	Gln	Val	Lys	Thr	Phe	Lys	Pro	Lys	Leu	Val
						115		120			125				

Ala	Val	Arg	Asn	Glu	Ser	Leu	Leu	Asn	Glu	Leu	Lys	Glu	Ala	Leu	Ala
						130		135			140				

Gly	Cys	Glu	Glu	Met	Pro	Glu	Ile	Ile	Pro	Gly	Glu	Gln	Gly	Val	Ile
						145		150			155			160	

Glu	Val	Ala	Arg	His	Pro	Asp	Ala	Val	Thr	Val	Val	Thr	Gly	Ile	Val
						165			170				175		

Gly	Cys	Ala	Gly	Leu	Lys	Pro	Thr	Val	Ala	Ala	Ile	Glu	Ala	Gly	Lys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

180	185	190
Asp Ile Ala Leu Ala Asn Lys Glu Thr Leu Ile Ala Gly Gly Pro Phe		
195	200	205
Val Leu Pro Leu Ala His Lys His Asn Val Lys Ile Leu Pro Ala Asp		
210	215	220
Ser Glu His Ser Ala Ile Phe Gln Cys Ile Gln Gly Leu Ser Glu Gly		
225	230	235
Ser Leu Arg Arg Val Ile Leu Thr Ala Ser Gly Gly Ala Phe Arg Asp		
245	250	255
Trp Pro Val Glu Lys Leu Lys Asp Val Lys Val Ala Asp Ala Leu Lys		
260	265	270
His Pro Asn Trp Ser Met Gly Lys Ile Thr Val Asp Ser Ala Thr		
275	280	285
Leu Phe Asn Lys Gly Leu Glu Val Ile Glu Ala His Tyr Leu Phe Gly		
290	295	300
Ala Glu Tyr Asp Asp Ile Glu Ile Val Ile His Pro Gln Ser Ile Ile		
305	310	315
His Ser Met Ile Glu Thr Gln Asp Ser Ser Val Leu Ala Gln Leu Gly		
325	330	335
Trp Pro Asp Met Arg Leu Pro Ile Leu Tyr Thr Leu Ser Trp Pro Asp		
340	345	350
Arg Val Tyr Cys Ser Glu Val Thr Trp Pro Arg Leu Asp Leu Cys Lys		
355	360	365
Leu Gly Ser Leu Thr Phe Lys Ala Pro Asp Asn Val Lys Tyr Pro Ser		
370	375	380
Val Asp Leu Ala Tyr Ala Ala Gly Arg Ala Gly Gly Thr Met Thr Gly		
385	390	395
400		
Val Leu Ser Ala Ala Asn Glu Lys Ala Val Glu Leu Phe Ile Asp Glu		
405	410	415
Lys Ile Ser Tyr Leu Asp Ile Phe Lys Val Val Glu Met Thr Cys Asp		
420	425	430
Ala His Arg Asn Glu Leu Val Thr Arg Pro Ser Leu Glu Glu Ile Ile		
435	440	445
His Tyr Asp Gln Trp Ala Arg Lys Phe Ala Ala Asn Leu Gln Pro Ser		
450	455	460
Ser Ser Gly Arg Ser Pro Val Leu Ala		
465	470	

<210> 21
<211> 406
<212> PRT
<213> Arabidopsis thaliana

<400> 21
 Ala Pro Arg Gln Ser Trp Asp Gly Pro Lys Pro Ile Ser Ile Val Gly
 1 5 10 15

 Ser Thr Gly Ser Ile Gly Thr Gln Thr Leu Asp Ile Val Ala Glu Asn
 20 25 30

 Pro Asp Lys Phe Arg Val Val Ala Leu Ala Ala Gly Ser Asn Val Thr
 35 40 45

 Leu Leu Ala Asp Gln Val Arg Arg Phe Lys Pro Ala Leu Val Ala Val
 50 55 60

 Arg Asn Glu Ser Leu Ile Asn Glu Leu Lys Glu Ala Leu Ala Asp Leu
 65 70 75 80

 Asp Tyr Lys Leu Glu Ile Ile Pro Gly Glu Gln Gly Val Ile Glu Val
 85 90 95

 Ala Arg His Pro Glu Ala Val Thr Val Val Thr Gly Ile Val Gly Cys
 100 105 110

 Ala Gly Leu Lys Pro Thr Val Ala Ala Ile Glu Ala Gly Lys Asp Ile
 115 120 125

 Ala Leu Ala Asn Lys Glu Thr Leu Ile Ala Gly Gly Pro Phe Val Leu
 130 135 140

 Pro Leu Ala Asn Lys His Asn Val Lys Ile Leu Pro Ala Asp Ser Glu
 145 150 155 160

 His Ser Ala Ile Phe Gln Cys Ile Gln Gly Leu Pro Glu Gly Ala Leu
 165 170 175

 Arg Lys Ile Ile Leu Thr Ala Ser Gly Gly Ala Phe Arg Asp Trp Pro
 180 185 190

 Val Glu Lys Leu Lys Glu Val Lys Val Ala Asp Ala Leu Lys His Pro
 195 200 205

 Asn Trp Asn Met Gly Lys Lys Ile Thr Val Asp Ser Ala Thr Leu Phe
 210 215 220

 Asn Lys Gly Leu Glu Val Ile Glu Ala His Tyr Leu Phe Gly Ala Glu
 225 230 235 240

 Tyr Asp Asp Ile Glu Ile Val Ile His Pro Gln Ser Ile Ile His Ser
 245 250 255

 Met Ile Glu Thr Gln Asp Ser Ser Val Leu Ala Gln Leu Gly Trp Pro
 260 265 270

 Asp Met Arg Leu Pro Ile Leu Tyr Thr Met Ser Trp Pro Asp Arg Val
 275 280 285

 Pro Cys Ser Glu Val Thr Trp Pro Arg Leu Asp Leu Cys Lys Leu Gly
 290 295 300

 Ser Leu Thr Phe Lys Lys Pro Asp Asn Val Lys Tyr Pro Ser Met Asp

305	310	315	320
Leu Ala Tyr Ala Ala Gly Arg Ala Gly Gly Thr Met Thr Gly Val Leu			
325	330	335	
Ser Ala Ala Asn Glu Lys Ala Val Glu Met Phe Ile Asp Glu Lys Ile			
340	345	350	
Ser Tyr Leu Asp Ile Phe Lys Val Val Glu Leu Thr Cys Asp Lys His			
355	360	365	
Arg Asn Glu Leu Val Thr Ser Pro Ser Leu Glu Glu Ile Val His Tyr			
370	375	380	
Asp Leu Trp Ala Arg Glu Tyr Ala Ala Asn Val Gln Leu Ser Ser Gly			
385	390	395	400
Ala Arg Pro Val His Ala			
405			
<210> 22			
<211> 475			
<212> PRT			
<213> Mentha x piperita			
<400> 22			
Met Ala Leu Asn Leu Met Ala Pro Thr Glu Ile Lys Thr Leu Ser Phe			
1	5	10	15
Leu Asp Ser Ser Lys Ser Asn Tyr Asn Leu Asn Pro Leu Lys Phe Gln			
20	25	30	
Gly Gly Phe Ala Phe Lys Arg Lys Asp Ser Arg Cys Thr Ala Ala Lys			
35	40	45	
Arg Val His Cys Ser Ala Gln Ser Gln Ser Pro Pro Pro Ala Trp Pro			
50	55	60	
Gly Arg Ala Phe Pro Glu Pro Gly Arg Met Thr Trp Glu Gly Pro Lys			
65	70	75	80
Pro Ile Ser Val Ile Gly Ser Thr Gly Ser Ile Gly Thr Gln Thr Leu			
85	90	95	
Asp Ile Val Ala Glu Asn Pro Asp Lys Phe Arg Ile Val Ala Leu Ala			
100	105	110	
Ala Gly Ser Asn Val Thr Leu Leu Ala Asp Gln Lys Ala Phe Lys Pro			
115	120	125	
Lys Leu Val Ser Val Lys Asp Glu Ser Leu Ile Ser Glu Leu Lys Glu			
130	135	140	
Ala Leu Ala Gly Phe Glu Asp Met Pro Glu Ile Ile Pro Gly Glu Gln			
145	150	155	160
Gly Met Ile Glu Val Ala Arg His Pro Asp Ala Val Thr Val Val Thr			
165	170	175	
Gly Ile Val Gly Cys Ala Gly Leu Lys Pro Thr Val Ala Ala Ile Glu			

180	185	190
Ala Gly Lys Asp Ile Ala Leu Ala Asn Lys Glu Thr Leu Ile Ala Gly		
195	200	205
Gly Pro Phe Val Leu Pro Leu Ala Lys Lys His Asn Val Lys Ile Leu		
210	215	220
Pro Ala Asp Ser Glu His Ser Ala Ile Phe Gln Cys Ile Gln Gly Leu		
225	230	235
240		
Pro Glu Gly Ala Leu Arg Arg Ile Ile Leu Thr Ala Ser Gly Gly Ala		
245	250	255
Phe Arg Asp Leu Pro Val Glu Lys Leu Lys Glu Val Lys Val Ala Asp		
260	265	270
Ala Leu Lys His Ser Asn Trp Asn Met Gly Lys Lys Asn Thr Val Arg		
275	280	285
Leu Leu Gln Leu Phe Phe Asn Lys Gly Leu Glu Val Ile Lys Ala His		
290	295	300
Tyr Leu Phe Gly Ala Glu Tyr Asp Asp Ile Glu Ile Val Ile His Ser		
305	310	315
320		
Pro Ser Ile Ile His Ser Met Val Glu Thr Gln Asp Ser Ser Val Leu		
325	330	335
Ala Gln Leu Gly Trp Pro Asp Met Arg Leu Pro Ile Leu Tyr Thr Leu		
340	345	350
Ser Trp Pro Glu Arg Val Tyr Cys Ser Glu Ile Thr Trp Pro Arg Leu		
355	360	365
Asp Leu Cys Lys Val Asp Leu Pro Phe Lys Lys Pro Asp Asn Arg Glu		
370	375	380
Ile Pro Ala Met Asp Leu Ala Tyr Ala Ala Trp Lys Ser Arg Ser Thr		
385	390	395
400		
Met Thr Gly Val Leu Ser Ala Ala Asn Glu Lys Ala Val Glu Met Phe		
405	410	415
Ile Asp Glu Lys Ile Gly Tyr Leu Asp Ile Phe Lys Val Val Glu Leu		
420	425	430
Thr Cys Asp Lys His Arg Ser Glu Met Ala Val Ser Pro Ser Leu Glu		
435	440	445
Glu Ile Val His Tyr Asp Gln Trp Ala Arg Asp Tyr Ala Ala Thr Val		
450	455	460
Leu Lys Ser Ala Gly Leu Ser Pro Ala Leu Val		
465	470	475